Factors impacting genomic testing rates among epithelial ovarian cancer patients across a large community-based healthcare system

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Factors impacting genomic testing rates among epithelial ovarian cancer patients across a large community-based healthcare system

Funded by AstraZeneca and Providence
Objective

To review the rates of germline and somatic biomarker testing for EOC patients and identify barriers to testing across a large community-based healthcare system operating in five states.

- Study population and data collection
  As described previously

- Data analysis
  - Descriptive statistics were tabulated
  - Multivariable logistic regression was used to summarize findings
Rates of Genomic Testing

- GMT: 508 patients
- Somatic TTT: 286 patients (28%)
- 221 patients

n=1015 patients
## Rates of Testing Across Ethnicity

<table>
<thead>
<tr>
<th>Race/Ethnicity</th>
<th>No Testing (N=1832)</th>
<th>Germine (N=508)</th>
<th>Somatic (N=221)</th>
<th>Germ.+Somatic (N=286)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, median (range)</td>
<td>63 (16, 100)</td>
<td>62 (21, 91)</td>
<td>64 (29, 89)</td>
<td>62 (24, 92)</td>
<td>0.3903</td>
</tr>
<tr>
<td>White or Caucasian</td>
<td>1292 (62%)</td>
<td>405 (19%)</td>
<td>166 (8%)</td>
<td>237 (11%)</td>
<td>0.0002</td>
</tr>
<tr>
<td>Hispanic or Latino</td>
<td>217 (75%)</td>
<td>37 (13%)</td>
<td>26 (9%)</td>
<td>9 (3%)</td>
<td></td>
</tr>
<tr>
<td>Asian</td>
<td>118 (68%)</td>
<td>24 (14%)</td>
<td>13 (8%)</td>
<td>18 (10%)</td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>116 (71%)</td>
<td>25 (15%)</td>
<td>9 (5%)</td>
<td>14 (9%)</td>
<td></td>
</tr>
<tr>
<td>Black or African American</td>
<td>53 (79%)</td>
<td>6 (9%)</td>
<td>3 (4%)</td>
<td>5 (7%)</td>
<td></td>
</tr>
<tr>
<td>American Indian/ Alaska Native</td>
<td>24 (62%)</td>
<td>9 (23%)</td>
<td>3 (8%)</td>
<td>3 (8%)</td>
<td></td>
</tr>
<tr>
<td>Native Hawaiian/ Pacific Islander</td>
<td>12 (80%)</td>
<td>2 (13%)</td>
<td>1 (7%)</td>
<td>0 (0%)</td>
<td></td>
</tr>
</tbody>
</table>
### Rates of Testing Based on Stage and Insurance status

<table>
<thead>
<tr>
<th>Stage at Diagnosis</th>
<th>No Testing (N=1832)</th>
<th>Germline (N=508)</th>
<th>Somatic (N=221)</th>
<th>Germ.+Somatic (N=286)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stage I</td>
<td>208 (71%)</td>
<td>67 (23%)</td>
<td>4 (1%)</td>
<td>16 (5%)</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Stage II</td>
<td>59 (63%)</td>
<td>22 (23%)</td>
<td>4 (4%)</td>
<td>9 (10%)</td>
<td></td>
</tr>
<tr>
<td>Stage III</td>
<td>217 (52%)</td>
<td>101 (24%)</td>
<td>41 (10%)</td>
<td>60 (14%)</td>
<td></td>
</tr>
<tr>
<td>Stage IV</td>
<td>139 (58%)</td>
<td>50 (21%)</td>
<td>14 (6%)</td>
<td>35 (15%)</td>
<td></td>
</tr>
<tr>
<td>Unknown</td>
<td>1209 (67%)</td>
<td>268 (15%)</td>
<td>158 (9%)</td>
<td>166 (9%)</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Insurance Status</th>
<th>No Testing (N=1832)</th>
<th>Germline (N=508)</th>
<th>Somatic (N=221)</th>
<th>Germ.+Somatic (N=286)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Medicare</td>
<td>666 (66%)</td>
<td>166 (17%)</td>
<td>71 (7%)</td>
<td>100 (10%)</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Commercial</td>
<td>463 (60%)</td>
<td>166 (21%)</td>
<td>48 (6%)</td>
<td>99 (13%)</td>
<td></td>
</tr>
<tr>
<td>Commercial +</td>
<td>256 (58%)</td>
<td>95 (22%)</td>
<td>42 (10%)</td>
<td>48 (11%)</td>
<td></td>
</tr>
<tr>
<td>Medicare/Medicaid</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Medicaid</td>
<td>240 (75%)</td>
<td>42 (13%)</td>
<td>22 (7%)</td>
<td>16 (5%)</td>
<td></td>
</tr>
<tr>
<td>No Insurance</td>
<td>123 (63%)</td>
<td>25 (13%)</td>
<td>32 (16%)</td>
<td>15 (8%)</td>
<td></td>
</tr>
<tr>
<td>Other Insurance</td>
<td>84 (75%)</td>
<td>14 (13%)</td>
<td>6 (5%)</td>
<td>8 (7%)</td>
<td></td>
</tr>
</tbody>
</table>
Somatic TTT was more frequent in patients with advanced stage disease

$X^2=34.8 \ p<.00001$
Rates of HRD in Patients who had Genomic Testing

<table>
<thead>
<tr>
<th>Category</th>
<th>All Pts Tested</th>
<th>I</th>
<th>II</th>
<th>III</th>
<th>IV</th>
<th>Unknown</th>
<th>Test Type</th>
<th>Germline</th>
<th>Somatic TTT</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1,015</td>
<td>87</td>
<td>35</td>
<td>202</td>
<td>99</td>
<td>592</td>
<td>n</td>
<td>794</td>
<td>507</td>
</tr>
<tr>
<td></td>
<td>10% 6% 4% 3%</td>
<td>7% 3% 1% 2%</td>
<td>6% 3% 3% 9%</td>
<td>10% 6% 5% 3%</td>
<td>12% 7% 3% 3%</td>
<td>10% 6% 5% 3%</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

BRCA1 BRCA2 LOH/GI Other HRR Genes
## Rates of Testing Based on Available Tissue Sample

<table>
<thead>
<tr>
<th>Surgical Procedures</th>
<th>No Testing (N=1832)</th>
<th>Germline (N=508)</th>
<th>Somatic (N=221)</th>
<th>Germ.+Somatic (N=286)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hysterectomy</td>
<td>634 (63%)</td>
<td>175 (17%)</td>
<td><strong>87 (9%)</strong></td>
<td><strong>116 (11%)</strong></td>
<td>0.004</td>
</tr>
<tr>
<td>Biopsy</td>
<td>34 (58%)</td>
<td>14 (24%)</td>
<td><strong>10 (17%)</strong></td>
<td><strong>1 (2%)</strong></td>
<td>0.004</td>
</tr>
<tr>
<td>Other (GI/IR/CV/Excisions)</td>
<td>526 (63%)</td>
<td>147 (18%)</td>
<td>68 (8%)</td>
<td>88 (11%)</td>
<td>0.004</td>
</tr>
<tr>
<td>None</td>
<td>638 (67%)</td>
<td>172 (18%)</td>
<td>56 (6%)</td>
<td>81 (9%)</td>
<td>0.004</td>
</tr>
</tbody>
</table>
Somatic TTT was more frequent in patients who had an available tissue sample by biopsy or hysterectomy.
## Rates of Testing Based on Clinical Setting

<table>
<thead>
<tr>
<th>Clinical Setting Type</th>
<th>No Testing (N=1832)</th>
<th>Germline (N=508)</th>
<th>Somatic (N=221)</th>
<th>Germ.+Somatic (N=286)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Academic</td>
<td>412 (58%)</td>
<td>104 (15%)</td>
<td>102 (14%)</td>
<td>92 (13%)</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>CoC</td>
<td>992 (64%)</td>
<td>312 (20%)</td>
<td>87 (6%)</td>
<td>171 (11%)</td>
<td></td>
</tr>
<tr>
<td>Community</td>
<td>428 (74%)</td>
<td>92 (16%)</td>
<td>32 (6%)</td>
<td>23 (4%)</td>
<td></td>
</tr>
</tbody>
</table>
Conclusions

• Within this cohort of 2847 patients, 36% (n= 1015 patients) completed some type of genomic testing

• The following factors influenced testing rate: Race/ethnicity, stage at diagnosis, insurance status, clinical setting type, and year of diagnosis

• The data highlight discrepancies in GT heavily influenced by practice setting, insurance status, and stage of diagnosis (likely reflecting payer coverage/ increased need for information in advanced stage disease).

• Of patients who received genomic testing, patients who received both germline and somatic testing increased from 26% in 2015 to 35% in 2019

• This study is the first to analyze rates of germline and somatic biomarker testing for EOC across a broad community-based healthcare system

• There is a need for a universally defined approach to provide equitable access to evidence based cancer care
Study Limitations

Only ovarian cancer patients were included, not fallopian or primary peritoneal

Histology was unknown in a majority of patients, hence this cohort over-estimates patients that would normally get testing

Somatic testing indications evolved during study timeframe

Approval for broad PARPi treatment in patients with HRD occurred during the study period
References


Acknowledgements

Commercial
Basia Gorska
Chris Koo
Julie Ramage
Laurie Stupakis
Shivani Vora

Medical
Nashwa Kabil
Julia Engstrom-Melnyk

Core team
Charles Drescher
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Fernanda Musa
Nicole Kretzer
Topher Darus

Health Research Accelerator
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Roshanthi Weerasinghe
Shwetha Pindikuri
Amy Parrish
Grace Li

Health Insights
Stephanie Christopher
Michele Wenzler
Next step: PSJH Ovarian Cancer Initiative – A reflex genetic/genomic testing protocol for ovarian cancer patients as part of a quality improvement initiative

Overall goal: implement a “reflex” molecular testing strategy for newly diagnosed ovarian cancer patients at high volume centers within the PSJH network
n=6 high centers (and 2-3 satellites) with a total of 400-500 cases annually

Objectives:
- Ensure that all newly diagnosed ovarian cancer patients receive clinically indicated germline and somatic testing
- Offer testing that is timely, convenient, and cost effective
  - Patients need to be fully informed re: indications and implications of various tests and have access to needed resources
- Develop databases and infrastructure to facilitate molecularly driven outcome studies in this population
  - Phase I - genotype/phenotype correlative study in over 1600 ovarian cancer cases
  - Phase II- perform large panel somatic sequencing for ALL EOC cases
**Reflex Germline Testing Protocol**

**Case Detection**
- Primary Treatment Team at diagnosis
- Site specific pathology script (weekly)- Prov CDW
  - GC/GCA
  - Project coordinator
- Patients provided link to Ambry CARE chatbot

**Pre-Test Education and Consent**
- Online Option: Ambry Genetics chatbot
  - Automated link provided to patient
  - Education and consent
  - Ambry handles insurance issues
  - Sends out test materials
  - Testing
    - Local clinic or lab
    - Drop-in clinic
    - Direct mail
    - Direct referral to GC services

**Testing and Post-Test Counseling**
- Results in 3-4 weeks
- Patients with neg result or VUS called with option for GC appointment
- Patients with mutations identified have GC visit scheduled
- Each step in the process tracked via Ambry Portal

Patient progress tracked in Ambry CARE tool
Ambry CARE chatbot

- Link sent to patient in email, myChart or via QR code in office
- Walks them through family history questions
- Works on phone or web browser
- Provides education videos
Reflex Somatic Testing Workflow
*(initiated in parallel with Germline Testing Workflow)*

**Case Detection**
- Primary Treatment Team or local Pathologist identifies case and places order
- All EOC cases
- Local pathologist pulls and ships relevant material to Providence Molecular Genomics Lab (MLG) - Portland

**Tumor Testing**
- Molecular Genomics Lab - Providence Portland
  - Illumina TSO NGS assay
  - 523 genes
  - Single pipeline for DNA/RNA analysis
  - All relevant molecular abnormalities plus TMB and MSI (PD-L1 optional)
  - and prepares and ships relevant material to Myriad for myChoice CDx - HRD

**Results Reporting**
- Integrated MGL/Myriad Report in MGL portal within 3-6 weeks of order
  - Includes all genomic variants and HRD/TMB/MSI
  - Highlights FDA approved mutational directed therapies
  - System-wide MTB
  - Genomics Navigator likely available for follow-up with treating physician

Patients identified via Epic staging or pathology report search tool and tracked in laboratory portals (aided by HRA)
Acknowledgements

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Julie Levine

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Patrick Foley  
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